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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2011; month=9; day=16; hr=15; min=14; sec=5; ms=683; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 1

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 1

Asn Gly Ser Phe Ser Gly Phe

1

5

Please remove the blank line between the above amino acids and their amino acid numbers. Amino acid numbers must appear directly below their amino acids. This error appears in all amino acid sequences in the submitted file.

To correct the sequence listing errors noted in this report - The recommended method for correction of errors is to access the sequence listing working file using the software program in which the listing was originally prepared, e.g., the project file in PatentIn, make any necessary corrections within that program, then generate a new sequence listing file. Use of a word processing program to correct errors directly in the original sequence listing file is strongly discouraged, since such programs often introduce unintended changes to the sequence listing, rendering the listing unacceptable. When the working file or original program is not available for correction, then use of a common or plain text-only editor, such as NotePad, to edit the original sequence listing file may suffice.

\*\*\*\*\*

Application No: 10579655 Version No: 6.0

Input Set:

Output Set:

**Started:** 2011-09-16 14:09:07.898  
**Finished:** 2011-09-16 14:09:29.750  
**Elapsed:** 0 hr(s) 0 min(s) 21 sec(s) 852 ms  
**Total Warnings:** 415  
**Total Errors:** 2984  
**No. of SeqIDs Defined:** 415  
**Actual SeqID Count:** 415

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)

**Input Set:**

**Output Set:**

**Started:** 2011-09-16 14:09:07.898  
**Finished:** 2011-09-16 14:09:29.750  
**Elapsed:** 0 hr(s) 0 min(s) 21 sec(s) 852 ms  
**Total Warnings:** 415  
**Total Errors:** 2984  
**No. of SeqIDs Defined:** 415  
**Actual SeqID Count:** 415

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E 321	No. of Bases conflict, this line has no nucleotides SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (10)

**Input Set:**

**Output Set:**

**Started:** 2011-09-16 14:09:07.898  
**Finished:** 2011-09-16 14:09:29.750  
**Elapsed:** 0 hr(s) 0 min(s) 21 sec(s) 852 ms  
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E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (12) POS (0)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

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<120> METHODS FOR PURIFYING PERTUSSIS TOXIN AND PEPTIDES USEFUL  
THEREFOR

<130> API-03-15

<140> 10579655

<141> 2011-09-16

<150> 60/523,881

<151> 2003-11-20

<150> PCT/US2004/038700

<151> 2004-11-18

<160> 415

<170> PatentIn version 3.5

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His Val Lys Arg Asp Ser Ser Pro Gly Ser Ile Asp Ala

<210> 7

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Asp Arg Pro His Arg Ser Arg Leu Ser Ile Asp Asp Asp Ala

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Cys Gly

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Cys Cys Glu Pro Leu Glu Cys Phe Gln Met Gly His Gly Phe Lys Arg

20 25 30

Cys Gly

<210> 11

<211> 35

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Cys Gly Ser

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<210> 12

<211> 34

<212> PRT

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Cys Gly

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<211> 35

<212> PRT

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Gln Gln Cys Val Lys Lys Asp Glu Leu Cys Ile Pro Tyr Tyr Leu Asp

1 5 10 15

Cys Cys Glu Pro Leu Glu Cys Lys Lys Val Asn Trp Trp Asp His Lys

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Cys Ile Gly

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nnsnnstgct gtgagcccct cgagtgcnnns nnsnnsnnsn nsnnnsnnsn snnstgcggc 120

agcggcagtt ctgggtctag c 141

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catagtggct caagtcagg atca 84

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20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp Ala Asn Ala Pro

35 40 45

Lys Ala Ser Ala Ile

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<210> 20

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<400> 20

His His His His His His

1 5

<210> 21

<211> 6

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Asp Ala Asn Ala Pro Lys

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snnsnnsnns nnsnnsnnsn nsnnnsnnsn snnsnnsnns nnsnnagatc tagcatgatg 120

atgatga 127

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catcatcatc atgctagatc t 81

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<212> DNA

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aattaaatag cggatgcctt cggagcgtta gc

32

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18

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

Val Lys Lys Asp Glu Leu Cys Ala Gly Ser Val Gly His Cys Cys Glu

20 25 30

Pro Leu Glu Cys Leu Arg Arg Phe Leu Asn Leu Arg Trp Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

Val Lys Lys Asp Glu Leu Cys Ile Val Met Arg Ala Pro Cys Cys Glu

20 25 30

Pro Leu Glu Cys Leu Arg Arg Tyr Met Leu Lys His Met Cys Gly Ser

35

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Gly Ser Ser Gly Ser Ser

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<210> 28

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<213> Artificial Sequence

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<223> Synthetic

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

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Val Lys Lys Asp Glu Leu Cys Lys Ala Phe Arg Tyr Ser Cys Cys Glu

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Pro Leu Glu Cys Leu Arg Lys Trp Leu Lys Ala Arg Phe Cys Gly Ser

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Gly Ser Ser Gly Ser Ser

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<210> 29

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

Val Lys Lys Asp Glu Leu Cys Leu Arg Ser Ser Ile Asp Cys Cys Glu

20 25 30

Pro Leu Glu Cys Leu Tyr Lys Trp Met Gln Arg Arg Leu Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

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<210> 30

<211> 54

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<213> Artificial Sequence

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<400> 30

Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

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Val Lys Lys Asp Glu Leu Cys Trp Pro Arg Arg His Lys Cys Cys Glu

20 25 30

Pro Leu Glu Cys Leu Leu Glu Met Leu Glu Arg Lys Arg Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

50

<210> 31

<211> 53

<212> PRT

<213> Artificial Sequence

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

Val Lys Lys Asp Glu Leu Cys Met Ser Met Ala Cys Val Cys Cys Glu

20 25 30

Pro Leu Glu Cys Lys Tyr His Gly Tyr Phe Trp Leu Cys Gly Ser Gly

35 40 45

Ser Ser Gly Ser Ser

50

<210> 32

<211> 54

<212> PRT

<213> Artificial Sequence

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

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Val Lys Lys Asp Glu Leu Cys Ala Val Trp Phe Asp Val Cys Cys Glu

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25

30

Pro Leu Glu Cys Thr Tyr Gln Ser Gly Tyr Tyr Trp Leu Cys Gly Ser

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Gly Ser Ser Gly Ser Ser

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<210> 33

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

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Val Lys Lys Asp Glu Leu Cys Glu Pro Trp Tyr Trp Arg Cys Cys Glu

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Pro Leu Glu Cys Val Tyr Thr Ser Gly Tyr Tyr Tyr Ser Cys Gly Ser

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Gly Ser Ser Gly Ser Ser

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20 25 30

Pro Leu Glu Cys Ile Tyr Thr Ser Glu Leu Tyr Ala Thr Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

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Val Lys Lys Asp Glu Leu Cys Val Phe Tyr Phe Pro Asn Cys Cys Glu

20 25 30

Pro Leu Glu Cys Arg Trp Val Asn Asp Asn Tyr Gly Trp Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

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<210> 36

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Val Lys Lys Asp Glu Leu Cys Met Ser Met Ala Cys Val Cys Cys Glu

20 25 30

Pro Leu Glu Cys Lys Tyr His Gly Tyr Phe Trp Leu Cys Gly Ser Gly

35 40 45

Ser Ser Gly Ser Ser

50

<210> 37

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Pro Leu Glu Cys Lys Trp Thr Asn Glu His Phe Gly Thr Cys Gly Ser

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Gly Ser Ser Gly Ser Ser

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25

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Pro Leu Glu Cys Lys Trp Phe Asn Glu Asn Tyr Gly Ile Cys Gly Ser

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Gly Ser Ser Gly Ser Ser

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<210> 39

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

Val Lys Lys Asp Glu Leu Cys Ala Arg Trp Asp Leu Val Cys Cys Glu

20 25 30

Pro Leu Glu Cys Ile Tyr Thr Ser Glu Leu Tyr Ala Thr Cys Gly Ser

35 40 45

Gly Ser Ser Gly Ser Ser

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Gly Ser Ser Gly Ser Ser

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Met His His His His His His Ser Gly Ser Ser Ser Gly Ser Gly Cys

1 5 10 15

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Pro Leu Glu Cys Tyr Tyr Thr Gly Trp Tyr Trp Ala Cys Gly Ser Gly

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Ser Ser Gly Ser Ser

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